

Software Analyzes Genetic Data and Matches Patients to Precision Drugs

wo landmark clinical trials, NCI Molecular Analysis for Therapy Choice (NCI-MATCH) and Pediatric MATCH, are ambitious for several reasons, not least of which is their aim to rapidly assess patients and treat them with therapies tailored to their specific cancers. In just two weeks, the trials screen DNA from patients' tumors, identify mutations, and assign patients to medicines that target those mutations.

This speedy timeline has been possible thanks in part to the Frederick National Laboratory, where a team of software engineers created and continue to update two analytical software platforms that match patients to the treatment that is best for them. The platforms, known as NCI-MATCHBox and PED-MATCHBox, are integral parts of the trials' approach to precision medicine—the practice of treating patients with medicines that target their individual traits, like genetic mutations.

Computing Enhances Clinical Efforts

Without the platforms, the trials would be forced to depend on traditional strategies for assigning treatments, such as committees of medical professionals who review each patient's genetic data and offer recommendations. That process would work, but it wouldn't keep pace with the two-week timeframe. Instead, the "computer doctor" inside NCI-MATCHBox and PED-MATCHBox quickly and reliably does the job.

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In reality, this doctor is a high-powered algorithm, a set of rules and mathematical formulae that analyzes the genetic data from each patient's tumor, curates the information, and recommends the relevant precision medicine. The strategic use of technology pairs patients with an appropriate treatment and frees up the trials' medical personnel to devote more attention to caring for patients and monitoring the treatments.

"The systems are highly accurate" said Brent D. Coffey, director of the Biomedical Applications Development Center at the Frederick National Laboratory. Coffey created the prototype for NCI-MATCHBox, assembled and led the engineering team that developed both platforms, and continues to oversee their maintenance and evolution.

The team built other crucial functions into NCI-MATCHBox and PED-MATCHBox in addition to the algorithm. At the platforms' heart is a data store containing information about the patients, their genetic data, and the precision drugs. The algorithm accesses these data to complete the analyses. There is also a workflow tool that helps the team enforce the trials' protocols, as well as a reporting engine that combines all data to assign patients to treatments. The parts work together to facilitate the trials.

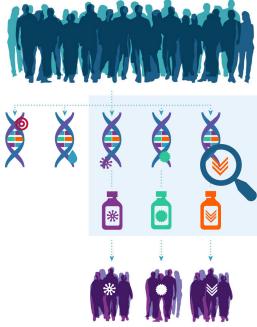


Brent Coffey, M.S., M.B.A.

Brent Coffey leads the Biomedical Applications Development Center at the Frederick National Laboratory.

Adaptability Foreshadows Future Success

Coffey and his colleagues continue to adjust NCI-MATCH-Box and PED-MATCHBox as the trials unfold, working on new algorithms central to new precision medicine research. With each change—workflow alterations, new drugs, new partnerships, and others—the team refines or redesigns entire portions of the software, so it remains current and accurate.



National Cancer Institute

The trials seek to determine whether precision medicines can be more broadly used in cancer treatments, and with the team's support, both are on track. NCI-MATCHBox and PED-MATCHBox maintain an accuracy rate of more than 98 percent, with the other 2 percent stemming mainly from minor data entry errors that have been corrected. With such an encouraging record, the platforms are expected to help scientists gain further insight into precision medicine and advance this area of clinical scholarship.

Collaborate with the Frederick National Laboratory

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